AMENDMENTS TO THE CLAIMS

This listing of claims replaces all prior versions, and listings, of claims in the application.

1.-85. (Canceled)

86. (Currently Amended) A method for detecting any species of the taxonomic unit of ~~enterobacteria~~ Enterobacteriaceae, and no species of another taxonomic unit, in an analytical sample, comprising the step of bringing the analytical sample into contact with an added nucleic acid or a combination of added nucleic acids, and detecting suitable hybrid nucleic acids comprising at least one of the added nucleic acids and a bacterial nucleic acid, wherein the one or more added nucleic acids are selected from the group consisting of:

a) nucleic acid molecules ~~comprising~~ consisting of at least one sequence of SEQ ID NOs: 2 ~~or~~ and 78;

~~b) nucleic acid molecules which hybridize specifically with SEQ ID NO: 2 or 78;~~

~~c)~~ b) nucleic acid molecules which exhibit at least ~~70%~~ 90% identity with a nucleic acid according to a); and

~~d)~~ c) nucleic acid molecules which are complementary to a nucleic acid ~~according to any~~ of a) ~~to c)~~ or b),

wherein any species of the taxonomic unit of Enterobacteriaceae, but no species of another taxonomic unit, is detected by formation of the hybrid nucleic acids.

87. (Canceled)

88. (Previously Presented) The method of claim 86, wherein the method involves a PCR amplification of the bacterial nucleic acid.

89. (Previously Presented) The method of claim 86, wherein the method involves a Southern Blot hybridization.

90. - 91. (Canceled)

92. (Currently Amended) A method for amplifying bacterial DNA of any species of the taxonomic unit of Enterobacteriaceae, comprising a first amplification step in which the DNA for a any species of the taxonomic unit of ~~the enterobacteria family~~ Enterobacteriaceae, and no species of another taxonomic unit is amplified with conserved primers to obtain a first amplification fragment, and, optionally, at least one further amplification step (EN) in which parts of the first amplification fragment, which are specific for ~~genera or~~ species of the taxonomic unit of Enterobacteriaceae, are multiplied with nested, increasingly variable primers, and, optionally, a further step in which the DNA fragments obtained by amplification, which are specific for ~~genera or~~ species of the taxonomic unit of Enterobacteriaceae, are detected by means of probes, wherein the primers used in the first amplification step comprise a nucleic acid selected from the group consisting of:

a) nucleic acid molecules ~~comprising~~ consisting of at least one sequence of the SEQ ID NOs: 2 and 78;

~~b) nucleic acid molecules which hybridize specifically with a nucleic acid according to a);~~

~~c)~~ b) nucleic acid molecules which exhibit at least ~~70%~~ 90% identity with a nucleic acid according to a); and

~~d)~~ c) nucleic acid molecules which are complementary to a nucleic acid ~~according to any~~ of a) ~~to c)~~ or b).

93. (Previously Presented) The method of claim 92, wherein the method involves a PCR amplification of the bacterial ~~nucleic acid~~ DNA.

94. (Previously Presented) A method according to claim 92, wherein the method involves a Southern Blot hybridization.

95.-96. (Canceled)

97. (Previously Presented) The method of claim 86, wherein the one or more added nucleic acid molecules are modified or labeled so that they can generate a signal for analytical detection, with the modification or labeling selected from the group consisting of (i) radioactive

groups, (ii) colored groups, (iii) fluorescent groups, (iv) groups for immobilization of a solid phase, and (v) groups which allow a direct or indirect reaction.

98. - 99. (Canceled)

100. (Currently Amended) A method for detecting any species of the taxonomic unit of Enterobacteriaceae, and no species of another taxonomic unit, ~~bacteria having a bacterial nucleic acid~~ in an analytical sample, comprising the step of bringing the analytical sample into contact with a combination of nucleic acids, and detecting suitable hybrid nucleic acids comprising one or more of the contacted nucleic acids and the bacterial nucleic acid, wherein the combination of nucleic acids comprises ~~a combination of~~ at least two nucleic acid molecules selected from the group consisting of:

a) ~~nucleic acid molecules comprising at least one sequence of SEQ ID NOs: 2 and 78;~~ a combination of a nucleic acid molecule consisting of SEQ ID NO: 2 and a nucleic acid molecule consisting of SEQ ID NO: 78;

~~b) nucleic acid molecules which hybridize specifically with any of SEQ ID NOs: 2 and 78;~~

~~c)~~ b) ~~nucleic acid molecules which exhibit 70% identity with a nucleic acid according to a)~~ a combination of a nucleic acid molecule which exhibits 90% identity with SEQ ID NO: 2, and a nucleic acid molecule which exhibits 90% identity with SEQ ID NO: 78; and

~~d)~~ c) ~~nucleic acid molecules which are complementary to a nucleic acid according to any of a) to c)~~ a combination of a nucleic acid molecules which are complementary to the combinations of a) or b),

wherein any species of the taxonomic unit of Enterobacteriaceae, but no species of another taxonomic unit, is detected by formation of the hybrid nucleic acids.

102.-104. (Cancelled)

105. (Currently Amended) A method for amplifying bacterial DNA of any species of the taxonomic unit of Enterobacteriaceae ~~of a multiplicity of different taxonomic units~~,

comprising a first amplification step in which the DNA for any species of the taxonomic ~~units~~ unit of ~~an enterobacteria family~~ Enterobacteriaceae, and no species of another taxonomic unit is amplified with conserved primers to obtain a first amplification fragment, and, optionally, at least one further amplification step (EN) in which parts of the first amplification fragment, which are specific for ~~genera or~~ species of the taxonomic unit of Enterobacteriaceae, are multiplied with nested, increasingly variable primers, and optionally, a further step in which the DNA fragments obtained by amplification, which are specific for ~~genera or~~ species of the taxonomic unit of Enterobacteriaceae, are detected by means of probes, wherein the primers used in the first amplification step comprise a combination of at least two nucleic acid molecules, selected from the group consisting of:

a) a combination of a nucleic acid molecule ~~comprising~~ consisting of SEQ ID NO: 2 ~~with~~ and a nucleic acid molecule ~~comprising~~ consisting of SEQ ID NO: 78;

~~b) a combination of a nucleic acid molecule which hybridizes specifically with SEQ ID NO: 2, with a nucleic acid that hybridizes specifically with SEQ ID NO: 78;~~

~~c)~~ b) a combination of a nucleic acid molecule of a nucleic acid which exhibits ~~70%~~ 90% identity with SEQ ID NO: 2, ~~with~~ and a nucleic acid which exhibits ~~70%~~ 90% identity with SEQ ID NO: 78, and;

~~d)~~ c) a combination of ~~a~~ nucleic acid molecules which are complementary to the combinations of a) ~~to~~ or ~~c)~~ b).

106. (Canceled)

107. (Previously Presented) The method of claim 97, wherein the groups which allow a direct or indirect reaction are selected from the group consisting of antibodies, antigens, enzymes, and substances with affinity to enzymes or enzyme complexes.